RAW SEQUENCE LISTING PATENT APPLICATION US/08/790,757...

DATE: 12/18/96 TIME: 14:31:40

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This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING 1 . ENTERED General Information: (1) (i) APPLICANT: Ponath, Paul D. 5 Ringler, Douglas J. 6 Jones, S. Tarran 7 Newman, Walter 8 Saldanha, Jos 9 Bendig, Mary M. 10 (ii) TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH Á4 7 11 12 INTEGRIN 13 14 (iii) NUMBER OF SEQUENCES: 63 15 16 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. 17 18 (B) STREET: Two Militia Drive 19 (C) CITY: Lexington 20 (D) STATE: Massachusetts 21 (E) COUNTRY: USA 22 (F) ZIP: 02173 23 24 (V) COMPUTER READABLE FORM: 25 (A) MEDIUM TYPE: Floppy disk 26 (B) COMPUTER: IBM PC compatible 27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 29 30 (vi) CURRENT APPLICATION DATA: 31 (A) APPLICATION NUMBER: 08/700,737 32 (B) FILING DATE: 15-AUG-1996 33 (C) CLASSIFICATION: 34 35 (viii) ATTORNEY/AGENT INFORMATION: 36 (A) NAME: Brook, David E. 37 (B) REGISTRATION NUMBER: 22,592 38 (C) REFERENCE/DOCKET NUMBER: LKS95-10 39 40 (ix) TELECOMMUNICATION INFORMATION: 41 (A) TELEPHONE: (617) 861-6240 42 (B) TELEFAX: (617) 861-9540 43 44 45

(2) INFORMATION FOR SEQ ID NO:1:

46

PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/08/700,737

DATE: 12/18/96 TIME: 14:31:43

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7	(i) SEQUENCE CHARACTERISTICS:														
8	(A) LENGTH: 494 base pairs														
.9 .0	(B) TYPE: nucleic acid (C) STRANDEDNESS: double														
1	(C) STRANDEDNESS: double														
52	(D) TOPOLOGY: linear														
53															
54															
55	(ix) FEATURE:														
56 57	(A) NAME/KEY: CDS														
58	(B) LOCATION: 13444														
59															
60															
61 62	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:														
63	TTACKRGWMK WCATGRRATG SASCTRKRTC ATYYTCTTCT TGGTATCAAC AGCTACAAGT	60													
64															
65 66	GTCCACTCCC AGGTCCAACT GCAGCAGCCT GGGGCTGAGC TTGTGAAGCC TGGGACTTCA	120													
67		180													
68	GTGAAGCTGT CCTGCAAGGG TTATGGCTAC ACCTTCACCA GCTACTGGAT GCACTGGGTG														
69	AAGCAGAGGC CTGGACAAGG CCTTGAGTGG ATCGGAGAGA TTGATCCTTC TGAGAGTAAT	240													
70		200													
71 72	ACTAACTACA ATCAAAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAT TTCCTCCAGC	300													
73		360													
74	ACAGCCTACA TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCGGTCTA CTATTGTGCA														
75	AGAGGGGGTT ACGACGGATG GGACTATGCT ATTGACTACT GGGGTCAAGG CACCTCAGTC	420													
76 77		480													
7 <i>1</i>	ACCGTCTCCT CAGCCAAAAC GACACCRYCN CSYKTMTMYC YYSBDNNCCC YKGRWSCYTG	400													
79		494													
80	GNNGAAGCTT GGGA														
81	(2) INFORMATION FOR SEQ ID NO:2:														
82 83															
84	(i) SEQUENCE CHARACTERISTICS:														
85	(A) LENGTH: 144 amino acids														
86	(B) TYPE: amino acid (C) STRANDEDNESS:														
87	(D) TOPOLOGY: linear														
88 89	(8)														
90															
91															
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93	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:														
94 95															
96	Met Xaa Xaa Xaa Xaa Ile Xaa Phe Leu Val Ser Thr Ala Thr Ser														
97	1 5														
98	Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys														
99	Val His Ser Gin val Gin 200 520 520 5														

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/700,737

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117		Tyr	Туг			Arg	GIY	GLY	120	, AUP	1		-	125	i			
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124	(2)	INF	'AMRC	rion	FOR	SEQ	ID I	10:3										
125	(2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS:																	
126		(i) SE	QUEN	CE CE	IARA	TER.	LSTI	33 ; 1 =-	~								
127	(A) LENGTH: 428 base pairs																	
128	(R) Type: nucleic acid																	
129	(C) STRANDEDNESS: double (D) TOPOLOGY: linear																	
130			(D) T	OPOL	OGY:	Line	ear										
131																		
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134		(ix) FE	ATUR	E:		·ana	•										
135			(A) N	AME/	KEY:	CDS	400										
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PAGE: 4

RAW SEQUENCE LISTING PATENT APPLICATION US/08/790,737

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179	CHARACTERISTICS:																		
180	(i) SEQUENCE CHARACTERISTICS:																		
181	(A) LENGTH: 137 amino acids																		
182	(B) TYPE: amino acid																		
183	(n) monorogy: linear																		
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PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/08/796,737

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215 216 217	(2)	INFO	RMATI	ON I	FOR	SEQ	ID N	0:5:										
218		(i)	SEQU	JENC	E CH	ARAC	TERI 5 ba	STIC se p	S: airs									
219 220			(B	TY	PE:	nucl	.eic	acid		•						4		
221			(C) ST	RAND	EDNE	SS:	doub	le							·	C	
222	(D) TOPOLOGY: linear																	
223 224																		
225										•								
226		(ix)	FEA'	TURE	: ME/K	EY:	CDS											
227 228	(A) NAME/KEY: CDS (B) LOCATION: 16435																	
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232 233	CGAT	TACT	AG T	CGAC	ATO	AA	TTC	CC1	r GTT	AGG	CTC	TTG	GTG	CTT	CTG	TTG Leu		51
234					Met	Ly	s Lei	1 PEC	va]	Arg	Let	ı Lev 145		reu	Leo	Leu		
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236	mm/C	TGG	Δጥጥ	сст	GTT	TCC	GGA	GGT	GAT	GTT	ĠTG	GTG	ACT	CAA	ACT	CCA		99
237 238	Phe	TGG Trp	Ile	Pro	Val	Ser	Gly	Gly	Asp	Val	Val	Val	Thr	Gln	Thr	Pro		
239	150	•				155					160					103		
240		TCC	ama	aam	ama	N.C.C	արդու	GGA	GAT	CAA	GTT	TCT	ATC	TCT	TGC	AGG		147
241 242	CTC	TCC Ser	CTG Len	Pro	Val	Ser	Phe	Gly	Asp	Gln	Val	Ser	Ile	Ser	- 4	Arg		
242	Leu	261	200		170					175					180			
244								3.CI	mam	ccc	አልሮ	ACC	ТАТ	TTG	TCT	TGG		195
245	TCT	AGT Ser	CAG	AGT	CTT	GCA	AAG	AGT	TAT	Glv	Asn	Thr	Tyr	Leu	Ser	Trp		
246 247	Ser	ser	GIN	185	Pea	AIG	Lys	502	190				_	195				
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249	TAC	CTG	CAC	AAG	CCT	GGC	CAG	TCT	CCA	CAG	CTC	CTC	ATC Tle	TAT	Glv	Ile		2.10
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252 253		AAC	AGA	TTT	TCT	GGG	GTG	CCA	GAC	AGG	TTC	AGT	GGC	AGT	GGT	TCA Ser		291
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